## SEQUENCE LISTING

<11	<i>I</i>	Adema Figdo	Cor , Go or, C lips,	osse Carl	J.											
<12	!0> N	1amma	aliar	n Ger	nes;	Rela	ited	Reac	gents	anc	d Met	hods	5			
<13	0> [	X105	51Q													
<14 <14																
<16	0> 9	)														
<17	0> F	aten	tIn	Ver.	2.0											
<21 <21	0> 1 1> 1 2> D 3> p	960	te													
	1> C		.(14	67)												
	0> 1 gggt	ggc	attt	ctgc	at t	cgaa	gaag	a at	ctga	gaga	aac	ctga	cgc	aggg	agc	57
atg Met 1	ggt Gly	atc Ile	tgg Trp	acc Thr 5	tca Ser	ggc Gly	act Thr	gat Asp	atc Ile 10	ttc Phe	cta Leu	agt Ser	ctt Leu	tgg Trp 15	gag Glu	105
att Ile	tac Tyr	gtg Val	tct Ser 20	cca Pro	aga Arg	agc Ser	ccc Pro	gga Gly 25	tgg Trp	atg Met	gac Asp	ttt Phe	atc Ile 30	cag Gln	cat His	153
ttg Leu	gga Gly	gtt Val 35	tgc Cys	tgt Cys	ttg Leu	gtt Val	gct Ala 40	ctt Leu	att Ile	tca Ser	gtg Val	ggc Gly 45	ctc Leu	ctg Leu	tct Ser	201
gtg Val	gcc Ala 50	gcc Ala	tgc Cys	tgg Trp	ttt Phe	ctg Leu 55	cca Pro	tca Ser	atc Ile	ata Ile	gcg Ala 60	gcc Ala	gct Ala	gcc Ala	tcc Ser	249
tgg Trp 65	att Ile	atc Ile	acg Thr	tgt Cys	gtt Val 70	ctg Leu	ctg Leu	tgt Cys	tgc Cys	tcc Ser 75	aag Lys	cat His	gca Ala	cga Arg	tgt Cys 80	297
ttt Phe	att Ile	ctt Leu	ctt Leu	gtc Val 85	ttt Phe	ctc Leu	tct Ser	tgt Cys	ggc Gly 90	ctg Leu	cgt Arg	gaa Glu	ggc Gly	agg Arg 95	aat Asn	345
gct Ala	ttg Leu	att Ile	gca Ala 100	gct Ala	ggc Gly	aca Thr	ggg Gly	atc Ile 105	gtc Val	atc Ile	ttg Leu	gga Gly	cac His 110	gta Val	gaa Glu	393

aat Asn	att	ttt Phe 115	His	aac Asn	ttt Phe	aaa Lys	ggt Gly 120	Leu	cta Leu	gat Asp	ggt Gly	atg Met 125	act Thr	tgc Cys	aac Asn	441
		Ala												aaa Lys		489
														agt Ser		537
														ctt Leu 175		585
agt Ser	ccc Pro	agc Ser	cat His 180	gtc Val	ctg Leu	gag Glu	gca Ala	cag Gln 185	cta Leu	aat Asn	gac Asp	agc Ser	aaa Lys 190	Gly	gaa Glu	633
gtc Val	ctg Leu	agc Ser 195	gtc Val	ttg Leu	tac Tyr	cag Gln	atg Met 200	gca Ala	aca Thr	acc Thr	aca Thr	gag Glu 205	gtg Val	ttg Leu	tcc Ser	681
														gtc Val		729
														ggt Gly		777
														gat Asp 255		825
				Gln	Gln	Arg		Cys	Val			Leu		aag Lys		873
														cct Pro		921
														cat His		969
tgc Cys 305	atc Ile	tgg Trp	gtg Val	ctg Leu	ttt Phe 310	gca Ala	gct Ala	gta Val	gat Asp	tat Tyr 315	ctg Leu	ctg Leu	tat Tyr	cgg Arg	ctc Leu 320	1017
att Ile	ttc Phe	tca Ser	gtg Val	agc Ser 325	aag Lys	cag Gln	ttt Phe	Gln	agc Ser 330	ttg Leu	cca Pro	ggg Gly	ttt Phe	gag Glu 335	gtt Val	1065

cac His	ttg Leu	aaa Lys	ctg Leu 340	cac His	gga Gly	gag Glu	aaa Lys	caa Gln 345	gga Gly	act Thr	caa Gln	gat Asp	att Ile 350	atc Ile	cat His	1113
gat Asp	tct Ser	tcc Ser 355	ttt Phe	aat Asn	ata Ile	tct Ser	gtg Val 360	ttt Phe	gaa Glu	ccc Pro	aac Asn	tgt Cys 365	atc Ile	cca Pro	aaa Lys	1161
cca Pro	aaa Lys 370	ttc Phe	ctt Leu	cta Leu	tct Ser	gag Glu 375	acc Thr	tgg Trp	gtt Val	cct Pro	ctc Leu 380	agt Ser	gtt Val	att Ile	ctt Leu	1209
ttg Leu 385	ata Ile	tta Leu	gtg Val	atg Met	ctg Leu 390	gga Gly	ctg Leu	ttg Leu	tcc Ser	tct Ser 395	atc Ile	ctt Leu	atg Met	caa Gln	ctt Leu 400	1257
aaa Lys	atc Ile	ctg Leu	gtg Val	tca Ser 405	gca Ala	tct Ser	ttc Phe	tac Tyr	ccc Pro 410	agc Ser	gtg Val	gag Glu	agg Arg	aag Lys 415	cgc Arg	1305
atc Ile	caa Gln	tat Tyr	ctg Leu 420	cat His	gca Ala	aag Lys	ctg Leu	ctt Leu 425	aaa Lys	aaa Lys	aga Arg	tca Ser	aag Lys 430	cag Gln	ccg Pro	1353
ctg Leu	GLY	gaa Glu 435	gtc Val	aaa Lys	aga Arg	Arg	ctg Leu 440	agt Ser	ctc Leu	tat Tyr	Leu	aca Thr 445	aag Lys	att Ile	cat His	1401
ttc Phe	tgg Trp : 450	ctt Leu	cca Pro	gtc Val	Leu	aaa Lys 1 455	atg Met	att Ile .	agg Arg	Lys	aag Lys 460	caa Gln 1	atg Met .	gac Asp	atg Met	1449
gca a Ala : 465	agt ( Ser <i>l</i>	gca ( Ala <i>I</i>	gac ( Asp :	Lys .	tca Ser 470	tgaga	agac	cc c	gact	actc	c tc	agcca	acat			1497
cgca	ccaa	ca at	tct	cttca	a ggi	ctac	ggat	ggca	agtca	act a	attca	atgc	eg ga	ataa	tagag	1557
															cctgg	
ttato	geete	cc tt	tcat	ctca	a aaq	gccaa	aga	gct	gccaç	ggt a	aaato	ggtta	at gt	ggt	ctatg	1677
ttcca	aaca	a ac	caca	atgat	ctt	gcct	gtg	tcac	caato	gta a	acaag	gacto	et ag	gctg	ggtcc	1737
cctgg	gtgat	g ag	rtttc	cagca	tag	gaata	atg	ttca	agga	aa a	igaaa	acga	ıa aa	cagt	ttaa	1797
															igcaa	
												cccc	c ac	aato	gtct	1917
ctttt	ctcc	c tg	ctcc	ctta	tta	aaga	act	cttt	ctga	aa c	cc					1960

<210> 2 <211> 470 <212> PRT <213> primate

<400> 2 Met Gly Ile Trp Thr Ser Gly Thr Asp Ile Phe Leu Ser Leu Trp Glu Ile Tyr Val Ser Pro Arg Ser Pro Gly Trp Met Asp Phe Ile Gln His Leu Gly Val Cys Cys Leu Val Ala Leu Ile Ser Val Gly Leu Leu Ser Val Ala Ala Cys Trp Phe Leu Pro Ser Ile Ile Ala Ala Ala Ser Trp Ile Ile Thr Cys Val Leu Leu Cys Cys Ser Lys His Ala Arg Cys Phe Ile Leu Leu Val Phe Leu Ser Cys Gly Leu Arg Glu Gly Arg Asn Ala Leu Ile Ala Ala Gly Thr Gly Ile Val Ile Leu Gly His Val Glu 100 Asn Ile Phe His Asn Phe Lys Gly Leu Leu Asp Gly Met Thr Cys Asn 120 Leu Arg Ala Lys Ser Phe Ser Ile His Phe Pro Leu Lys Lys Tyr 135 Ile Glu Ala Ile Gln Trp Ile Tyr Gly Leu Ala Thr Pro Leu Ser Val 150 Phe Asp Asp Leu Val Ser Trp Asn Gln Thr Leu Ala Val Ser Leu Phe 165 170 Ser Pro Ser His Val Leu Glu Ala Gln Leu Asn Asp Ser Lys Gly Glu 180 185 Val Leu Ser Val Leu Tyr Gln Met Ala Thr Thr Thr Glu Val Leu Ser 200 Ser Leu Gly Gln Lys Leu Leu Ala Phe Ala Gly Leu Ser Leu Val Leu 215 Leu Gly Thr Gly Leu Phe Met Lys Arg Phe Leu Gly Pro Cys Gly Trp 225 230 Lys Tyr Glu Asn Ile Tyr Ile Thr Arg Gln Phe Val Gln Phe Asp Glu 250 Arg Glu Arg His Gln Gln Arg Pro Cys Val Leu Pro Leu Asn Lys Glu 265 Glu Arg Arg Lys Tyr Val Ile Ile Pro Thr Phe Trp Pro Thr Pro Lys

Glu Arg Lys Asn Leu Gly Leu Phe Phe Leu Pro Ile Leu Ile His Leu

290 295 300

Cys Ile Trp Val Leu Phe Ala Ala Val Asp Tyr Leu Leu Tyr Arg Leu 305 310 315 320

Ile Phe Ser Val Ser Lys Gln Phe Gln Ser Leu Pro Gly Phe Glu Val 325 330 335

His Leu Lys Leu His Gly Glu Lys Gln Gly Thr Gln Asp Ile Ile His 340 345 350

Asp Ser Ser Phe Asn Ile Ser Val Phe Glu Pro Asn Cys Ile Pro Lys 355 360 365

Pro Lys Phe Leu Leu Ser Glu Thr Trp Val Pro Leu Ser Val Ile Leu 370 375 380

Leu Ile Leu Val Met Leu Gly Leu Leu Ser Ser Ile Leu Met Gln Leu 385 390 395 400

Lys Ile Leu Val Ser Ala Ser Phe Tyr Pro Ser Val Glu Arg Lys Arg
405 410 415

Ile Gln Tyr Leu His Ala Lys Leu Leu Lys Lys Arg Ser Lys Gln Pro
420 425 430

Leu Gly Glu Val Lys Arg Arg Leu Ser Leu Tyr Leu Thr Lys Ile His 435 440 445

Phe Trp Leu Pro Val Leu Lys Met Ile Arg Lys Lys Gln Met Asp Met 450 455 460

Ala Ser Ala Asp Lys Ser 465 470

<210> 3

<211> 1410

<212> DNA

<213> Artificial Sequence

<220>

<220>

<221> misc\_feature

<222> (1)..(1410)

<223> n may be a, c, g, or t

<400> 3

atgggnatht ggacnwsngg nacngayath ttyytnwsny tntgggarat htaygtnwsn 60 ccnmgnwsnc cnggntggat ggayttyath carcayytng gngtntgytg yytngtngcn 120 ytnathwsng tnggnytnyt nwsngtngcn gcntgytggt tyytnccnws nathathgcn 180

gengengenw sntggathat haentgygtn ytnytntgyt gywsnaarca ygenmgntgy 240 ttyathytny tngtnttyyt nwsntgyggn ytnmgngarg gnmgnaaygc nytnathgcn 300 genggnaeng gnathgtnat hytnggneay gtngaraaya thttycayaa yttyaarggn 360 ytnytngayg gnatgacntg yaayytnmgn gcnaarwsnt tywsnathca yttyccnytn 420 ytnaaraart ayathgargc nathcartgg athtayggny tngcnacncc nytnwsngtn 480 ttygaygayy tngtnwsntg gaaycaracn ytngcngtnw snytnttyws nccnwsncay 540 gtnytngarg cncarytnaa ygaywsnaar ggngargtny tnwsngtnyt ntaycaratg 600 gcnacnacna cngargtnyt nwsnwsnytn ggncaraary tnytngcntt ygcnggnytn 660 wsnytngtny tnytnggnac nggnytntty atgaarmgnt tyytnggncc ntgyggntgg 720 aartaygara ayathtayat hacnmgncar ttygtncart tygaygarmg ngarmgncay 780 carcarmgnc cntgygtnyt nccnytnaay aargargarm gnmgnaarta ygtnathath 840 conacnttyt ggccnacncc naargarmgn aaraayytng gnytnttytt yytnocnath 900 ytnathcayy tntgyathtg ggtnytntty gcngcngtng aytayytnyt ntaymgnytn 960 athttywsng tnwsnaarca rttycarwsn ytnccnggnt tygargtnca yytnaarytn 1020 cayggngara arcarggnac ncargayath athcaygayw snwsnttyaa yathwsngtn 1080 ttygarccna aytgyathcc naarccnaar ttyytnytnw sngaracntg ggtnccnytn 1140 wsngtnathy tnytnathyt ngtnatgytn ggnytnytnw snwsnathyt natgcarytn 1200 aarathytng tnwsngcnws nttytayccn wsngtngarm gnaarmgnat hcartayytn 1260 caygcnaary tnytnaaraa rmgnwsnaar carcenytng gngargtnaa rmgnmgnytn 1320 wsnythtayy thachaarat heayttytgg ytheengthy thaaratgat hmghaaraar 1380 caratggaya tggcnwsngc ngayaarwsn 1410

```
<210> 4
<211> 942
<212> DNA
<213> primate

<220>
<221> CDS
<222> (1)..(939)

<220>
<221> mat_peptide
<222> (64)..(939)
```

<400> 4

ato Met	g gco Ala -20	a Let	a cca ı Pro	a gto Val	g aco	c gcc Ala -15	ı Leı	g cto 1 Lei	c cto 1 Lei	g cc	g cta o Lei -10	ı Ala	c tto a Lei	g cto u Lei	g ctc ı Leu	48
cac His -5	: Ala	c gcc a Ala	ago Aro	g cco g Pro -1	Asp	Tyr	aag Lys	g gad s Asp	gat Asp	Asp	c gad o Asp	c aag o Lys	g ato s Ile	c gat e Asp 10	ctg Leu )	96
ago Ser	aaa Lys	tgc Cys	agg Arg 15	f Thr	gtg Val	gcg Ala	ggc	e ccc Pro 20	Val	. Gly	g gga / Gly	tcc Ser	cto Leu 25	ı Ser	gtg Val	144
cag Gln	tgt Cys	ccc Pro 30	Tyr	gag Glu	aag Lys	gaa Glu	cac His 35	Arg	acc Thr	cto Leu	aac Asn	aaa Lys 40	Tyr	tgg Trp	tgc Cys	192
aga Arg	cca Pro 45	Pro	cag Gln	att	ttc Phe	cta Leu 50	tgt Cys	gac Asp	aag Lys	att	gtg Val	Glu	acc Thr	: aaa Lys	ggg Gly	240
tca Ser 60	gca Ala	gga Gly	aaa Lys	agg Arg	aac Asn 65	ggc Gly	cga Arg	gtg Val	tcc Ser	ato Ile 70	Arg	gac Asp	agt Ser	cct Pro	gca Ala 75	288
aac Asn	ctc Leu	agc Ser	ttc Phe	aca Thr 80	gtg Val	acc Thr	ctg Leu	gag Glu	aat Asn 85	ctc Leu	aca Thr	gag Glu	gag Glu	gat Asp 90	gca Ala	336
ggc Gly	acc Thr	tac Tyr	tgg Trp 95	tgt Cys	ggg Gly	gtg Val	gat Asp	aca Thr 100	ccg Pro	tgg Trp	ctc Leu	cga Arg	gac Asp 105	ttt Phe	cat His	384
gat Asp	ccc Pro	gtt Val 110	gtc Val	gag Glu	gtt Val	gag Glu	gtg Val 115	tcc Ser	gtg Val	ttc Phe	ccg Pro	gca Ala 120	tca Ser	acg Thr	tca Ser	432
atg Met	aca Thr 125	cct Pro	gca Ala	agt Ser	atc Ile	act Thr 130	gcg Ala	gcc Ala	aag Lys	acc Thr	tca Ser 135	aca Thr	atc Ile	aca Thr	act Thr	480
gca Ala 140	ttt Phe	cca Pro	cct Pro	gta Val	tca Ser 145	tcc Ser	act Thr	acc Thr	ctg Leu	ttt Phe 150	gca Ala	gtg Val	ggt Gly	gcc Ala	acc Thr 155	528
cac His	agt Ser	gcc Ala	agc Ser	atc Ile 160	cag Gln	gag Glu	gaa Glu	act Thr	gag Glu 165	gag Glu	gtg Val	gtg Val	aac Asn	tca Ser 170	cag Gln	576
ctc Leu	ccg Pro	Leu	ctc Leu 175	ctc Leu	tcc Ser	ctg Leu	Leu	gca Ala 180	ttg Leu	ttg Leu	ctg Leu	Leu	ctg Leu 185	ttg Leu	gtg Val	624
ggg .	Ala	tcc Ser 190	ctg Leu	cta Leu	gcc Ala	Trp 1	agg Arg : 195	atg Met	ttt Phe	cag Gln	Lys	tgg Trp 200	atc Ile	aaa Lys	gct Ala	672
ggt	gac	cat	tca	gag	ctg	tcc (	cag .	aac	ccc	aag	cag	gct	gcc	acg	cag	720

Gly	/ Asp 205	His	Ser	Glu	ı Leu	Ser 210		ı Asn	n Pro	Lys	Glr 215		Ala	ı Thr	Gln	
agt Ser 220	Glu	ı ctg ı Leu	cac His	tac Tyr	gca Ala 225	Asr	ctg Leu	gag Glu	r ctg Leu	cto Lev 230	Met	tgg Trp	cct Pro	ctg Leu	cag Gln 235	768
ga <i>a</i> Glu	aaç Lys	cca Pro	gca Ala	cca Pro 240	Pro	agg Arg	gag Glu	gtg Val	gag Glu 245	Val	gaa Glu	tac Tyr	agc Ser	act Thr 250		816
gcc Ala	tcc Ser	ccc	agg Arg 255	Glu	gaa Glu	ctt Leu	cac His	tat Tyr 260	Ala	tcg Ser	gtg Val	gtg Val	ttt Phe 265	gat Asp	tct Ser	864
aac Asn	acc Thr	aac Asn 270	agg Arg	ata Ile	gct Ala	gct Ala	cag Gln 275	agg Arg	cct Pro	cgg Arg	gag Glu	gag Glu 280	gaa Glu	cca Pro	gat Asp	912
tca Ser	gat Asp 285	tac Tyr	agt Ser	gtg Val	ata Ile	agg Arg 290	aag Lys	aca Thr	tag							942
<21 <21	0> 5 1> 3 2> P: 3> p:	RT														
	J. P.	LIMa	_e													
<40	0> 5			Val	Thr	Ala -15	Leu	Leu	Leu	Pro	Leu -10	Ala	Leu	Leu	Leu	
<40 Met	0> 5 Ala -20	Leu	Pro			-15	Leu Lys				-10					
<40 Met His -5	0> 5 Ala -20 Ala	Leu Ala	Pro Arg	Pro -1	Asp 1	-15 Tyr		Asp	Asp 5	Asp	-10 Asp	Lys	Ile	Asp 10	Leu	
<400 Met His -5 Ser	O> 5 Ala -20 Ala Lys	Leu Ala Cys	Pro Arg Arg 15	Pro -1 Thr	Asp 1 Val	-15 Tyr Ala	Lys	Asp Pro 20	Asp 5 Val	Asp	-10 Asp Gly	Lys Ser	Ile Leu 25	Asp 10 Ser	Leu Val	
<400 Met His -5 Ser	O> 5 Ala -20 Ala Lys	Leu Ala Cys Pro 30	Pro Arg Arg 15	Pro -1 Thr	Asp 1 Val Lys	-15 Tyr Ala Glu	Lys Gly His	Asp Pro 20 Arg	Asp 5 Val Thr	Asp Gly Leu	-10 Asp Gly Asn	Lys Ser Lys 40	Ile Leu 25 Tyr	Asp 10 Ser Trp	Leu Val Cys	
<400 Met His -5 Ser Gln	O> 5 Ala -20 Ala Lys Cys Pro 45	Leu Ala Cys Pro 30	Pro Arg Arg 15 Tyr	Pro -1 Thr Glu	Asp 1 Val Lys	-15 Tyr Ala Glu Leu 50	Lys Gly His 35	Asp Pro 20 Arg Asp	Asp 5 Val Thr	Asp Gly Leu Ile	-10 Asp Gly Asn Val 55	Lys Ser Lys 40 Glu	Ile Leu 25 Tyr Thr	Asp 10 Ser Trp Lys	Leu Val Cys Gly	
<400 Met His -5 Ser Gln Arg	O> 5 Ala -20 Ala Lys Cys Pro 45 Ala	Leu Ala Cys Pro 30 Pro Gly	Pro Arg Arg 15 Tyr Gln Lys	Pro -1 Thr Glu Ile	Asp 1 Val Lys Phe Asn 65	-15 Tyr Ala Glu Leu 50 Gly	Lys Gly His 35 Cys	Asp Pro 20 Arg Asp	Asp 5 Val Thr Lys Ser	Asp Gly Leu Ile 70	-10 Asp Gly Asn Val 55 Arg	Lys Ser Lys 40 Glu Asp	Ile Leu 25 Tyr Thr .	Asp 10 Ser Trp Lys	Leu Val Cys Gly Ala 75	
<400 Met His -5 Ser Gln Arg Ser 60 Asn	O> 5 Ala -20 Ala Lys Cys Pro 45 Ala	Leu Ala Cys Pro 30 Pro Gly Ser	Pro Arg Arg 15 Tyr Gln Lys Phe	Pro -1 Thr Glu Ile Arg	Asp 1 Val Lys Phe Asn 65 Val	-15 Tyr Ala Glu Leu 50 Gly Thr	Lys Gly His 35 Cys Arg Leu Asp	Asp Pro 20 Arg Asp Val Glu	Asp 5 Val Thr Lys Ser Asn 85	Asp Gly Leu Ile 70 Leu	-10 Asp Gly Asn Val 55 Arg	Lys Ser Lys 40 Glu Asp Glu Arg	Ile Leu 25 Tyr Thr . Ser	Asp 10 Ser Trp Lys Pro Asp 90	Leu Val Cys Gly Ala 75	

Met Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr 125 130 Ala Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr 145 150 His Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser Gln 160 Leu Pro Leu Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Val 180 Gly Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala 195 Gly Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln Ala Ala Thr Gln 210 215 Ser Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met Trp Pro Leu Gln 225 Glu Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu Tyr Ser Thr Val 240 245 Ala Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val Val Phe Asp Ser 255 260 Asn Thr Asn Arg Ile Ala Ala Gln Arg Pro Arg Glu Glu Glu Pro Asp 275 Ser Asp Tyr Ser Val Ile Arg Lys Thr <210> 6 <211> 603 <212> DNA <213> primate <220> <221> CDS <222> (1)..(600) <220> <221> mat\_peptide <222> (64)..(600) <400> 6 atg gcc tta cca gtg acc gcc ttg ctc ctg ccg cta gcc ttg ctc Met Ala Leu Pro Val Thr Ala Leu Leu Pro Leu Ala Leu Leu Leu -15cac gcc gcc agg ccg gat tac aag gac gat gac gac aag atc gat atg 96 His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Lys Ile Asp Met 10 aca cct gca agt atc act gcg gcc aag acc tca aca atc aca act gca

Thr	Pro	Ala	Ser 15		Thr	Ala	Ala	Lys 20		Ser	Thr	Ile	Thr 25		Ala	,
ttt Phe	cca Pro	cct Pro 30	gta Val	tca Ser	tcc Ser	act Thr	acc Thr 35	ctg Leu	ttt Phe	gca Ala	gtg Val	ggt Gly 40	gcc Ala	acc Thr	cac His	192
agt Ser	gcc Ala 45	agc Ser	atc Ile	cag Gln	gag Glu	gaa Glu 50	act Thr	gag Glu	gag Glu	gtg Val	gtg Val 55	aac Asn	tca Ser	cag Gln	ctc Leu	240
ccg Pro 60	ctg Leu	ctc Leu	ctc Leu	tcc Ser	ctg Leu 65	ctg Leu	gca Ala	ttg Leu	ttg Leu	ctg Leu 70	ctt Leu	ctg Leu	ttg Leu	gtg Val	ggg Gly 75	288
gcc Ala	tcc Ser	ctg Leu	cta Leu	gcc Ala 80	tgg Trp	agg Arg	atg Met	ttt Phe	cag Gln 85	aaa Lys	tgg Trp	atc Ile	aaa Lys	gct Ala 90	ggt Gly	336
gac Asp	cat His	tca Ser	gag Glu 95	ctg Leu	tcc Ser	cag Gln	aac Asn	ccc Pro 100	aag Lys	cag Gln	gct Ala	gcc Ala	acg Thr 105	cag Gln	agt Ser	384
gag Glu	ctg Leu	cac His 110	tac Tyr	gca Ala	aat Asn	ctg Leu	gag Glu 115	ctg Leu	ctg Leu	atg Met	tgg Trp	cct Pro 120	ctg Leu	cag Gln	gaa Glu	432
aag Lys	cca Pro 125	gca Ala	cca Pro	cca Pro	agg Arg	gag Glu 130	gtg Val	gag Glu	gtg Val	gaa Glu	tac Tyr 135	agc Ser	act Thr	gtg Val	gcc Ala	480
tcc Ser 140	ccc Pro	agg Arg	gaa Glu	gaa Glu	ctt Leu 145	cac His	tat Tyr	gcc Ala	tcg Ser	gtg Val 150	gtg Val	ttt Phe	gat Asp	tct Ser	aac Asn 155	528
acc Thr	aac Asn	agg Arg	ata Ile	gct Ala 160	gct Ala	cag Gln	agg Arg	cct Pro	cgg Arg 165	gag Glu	gag Glu	gaa Glu	cca Pro	gat Asp 170	tca Ser	576
gat Asp								tag								603

<210> 7 <211> 200

<212> PRT

<213> primate

<400> 7

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu -20 -15 -10

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Ile Asp Met -5 10

Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr Ala

15 20 25

Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr His 30 35 40

Ser Ala Ser Ile Gl<br/>n Glu Glu Thr Glu Glu Val Val As<br/>n Ser Gl<br/>n Leu 45 50 55

Pro Leu Leu Leu Ser Leu Leu Leu Leu Leu Leu Leu Leu Val Gly 60 70 75

Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala Gly 80 85 90

Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln Ala Ala Thr Gln Ser 95  $\phantom{\bigg|}100\phantom{\bigg|}105\phantom{\bigg|}$ 

Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met Trp Pro Leu Gl<br/>n Glu 110 115 120

Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu Tyr Ser Thr Val Ala 125 130 135

Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val Val Phe Asp Ser Asn 140 145 150 155

Thr Asn Arg Ile Ala Ala Gln Arg Pro Arg Glu Glu Glu Pro Asp Ser 160 165 170

Asp Tyr Ser Val Ile Arg Lys Thr 175

<210> 8

<211> 939

<212> DNA

<213> Artificial Sequence

<220>

<220>

<221> misc\_feature

<222> (1)..(939)

<223> n may be a, c, g, or t

<400> 8

atggenytne engtnaenge nytnytnytn eenytngeny tnytnytnea ygengenmgn 60 cengaytaya argaygayga ygayaarath gayytnwsna artgymgnae ngtngenggn 120 cengtnggng gnwsnytnws ngtneartgy eentaygara argareaymg naenytnaay 180 aartaytggt gymgneence nearathtty ytntgygaya arathgtnga raenaarggn 240 wsngenggna armgnaaygg nmgngtnwsn athmgngayw sneengenaa yytnwsntty 300

acngtnacny tngaraayyt nacngargar gaygenggna entaytggtg yggngtngay 360 aeneentggy tnmgngaytt yeaygayeen gtngtngarg tngargtnws ngtnttyeen 420 genwsnacnw snatgaenee ngenwsnath aengengena araenwsnae nathaenaen 480 genttyeene engtnwsnws nacnaenytn ttygengtng gngenaenea ywsngenwsn 540 atheargarg araengarga rgtngtnaay wsnearytne enytnytnyt nwsnytnytn 600 genytnytny tnytnytt ngtnggngen wsnytnytng entggmgnat gttyearaar 660 tggathaarg enggngayea ywsngarytn wsnearaaye enaarearge ngenaenear 720 wsngarytne aytaygenaa yytngarytn ytnatgtgge enytnearga raareengen 780 eeneenmgng argtngargt ngartaywsn aengtngenw sneenmgnga rgarytneay 840 taygenwsng tngtnttyga ywsnaayaen aaymgnathg engenearmg neenmgngar 900 gargareeng aywsngayta ywsngtnath mgnaaraen

```
<210> 9
<211> 600
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:reverse translation
<220>
<221> misc_feature
<222> (1)..(600)
<223> n may be a, c, g, or t
<400> 9
```

atggenytne engtnaenge nytnytnytn eenytngeny tnytnytnea ygengenmgn 60 cengaytaya argaygayga ygayaarath gayatgaene engenwsnat haengengen 120 aaraenwsna enathaenae ngenttyeen eengtnwsnw snaenaenyt nttygengtn 180 ggngenaene aywsngenws natheargar garaengarg argtngtnaa ywsnearytn 240 eenytnytny tnwsnytnyt ngenytnytn ytnytnytny tngtnggnge nwsnytnytn 300 gentggmgna tgttyearaa rtggathaar genggngaye aywsngaryt nwsnearaay 360 eenaarearg engenaenea rwsngarytn eaytaygena ayytngaryt nytnatgtgg 420 eenytnearg araareenge neeneenmgn gargtngarg tngartayws naengtngen 480 wsneenmgng argarytnea ytaygenwsn gtngtnttyg aywsnaayae naaymgnath 540

gengenearm gneenmgnga rgargareen gaywsngayt aywsngtnat hmgnaaraen 600